

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Ceriani, Roberto L.  
Peterson, Jerry A.  
Larocca, David J.
- (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON  
HMFG DIFFERENTIATION ANTIGEN  
BINDING SPECIFICITY, COMPOSITION,  
KIT & METHODS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Ratner & Prestia  
(B) STREET: Suite 301  
One Westlakes, Berwyn  
(C) CITY: Valley Forge  
(D) STATE: Pennsylvania  
(E) COUNTRY: USA  
(F) ZIP: 19482
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk 3.5"  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
(D) SOFTWARE: PatentIn #1.0,  
Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: January 2, 2002  
(C) CLASSIFICATION:
- PARENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/482,596  
(B) FILING DATE: June 7, 1995  
(C) CLASSIFICATION:
- grand parent APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/607,538  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Amzel, Viviana  
(B) REGISTRATION No.: 30,930  
(C) REFERENCE/DOCKET No: CRFC-047
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (610) 407-0700

(B) TELEFAX: (610) 407-0701  
(C) TELEX: N.A.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

62  
GATTTTCATCC ATGATGTTAA TAAAAAACAC AAGGAGTTTG TGGGTAAGT 50  
GAACAAAAAC GCGGTGCATG TCAACCTGTT TGAGACCCCT GTGGAGGCTC 100  
AGTACGTGAG ATTGTACCCC ACGAGCTGCC ACACGGCCTG CACTCTGCGC 150  
TTTGAGCTAC TGGGCTGTGA GCTGAACGGA TGCGCCAATC CCCTGGGCTC 200  
GAAGAATAAC AGCATCCCTG ACAAGCAGAT CACGGCCTCC AGCAGCTACA 250  
AGACCTGGGG CTTGCATCTC TTCAGCTGGA ACCCCTCCTA TGCACGGCTG 300  
GACAAGCAGG GCAACTTCAA CGCCTGGGTT GCGGGGAGCT ACGGTAACGA 350  
TCAGTGGCTG CAGGTGGACC TGGGCTCCTC GAAGGAGGTG ACAGGCATCA 400  
TCACCCAGGG GGCCCGTAAC TTTGGCTCTG TCCAGTTTGT GGCATCCTAC 450  
AAGGTTGCCT ACAGTAATGA CAGTGCGAAC TGGACTGAGT ACCAGGACCC 500  
CAGGACTGGC AGCAGTAAGA TCTTCCCTGG CAACTGGGAC AACCCTCCC 550  
ACAAGAAGAA CTGTGTTGAG ACGCCCATCC TGGCTCGCTA TGTGCGCATC 600  
CTGCCTGTAG CCTGGCACAA CCGCATCGCC CTGCGCCTGG AGCTGCTGGG 650  
CTGTTAGTGG CCACCTGCCA CCCCAGGTC TTCCTGCTTT CCATGGGCCC 700  
GCTGCCTCTT GGCTTCTCAG CCCCTTTAAA TCACCATAGG GCTGGGGACT 750  
GGGGAAGGGG AGGGTGTTCA GAGGCAGCAC CACCACACAG TCACCCCTCC 800  
CTCCCTCTTT CCCACCCTCC ACCTCTCACG GGCCCTGCCC CAGCCCCTAA 850  
GCCCCGTCCC CTAACCCCCA GTCCTCACTG TCCTGTTTTT TTAGGCACTG 900  
AGGGATCTGA GTAGGTCTGG GATGGACAGG AAAGGGCAAA GTAGGGCGTG 950  
TGTTTCCCTT GCCCTGTCC GGACCGCCGA TCCCAGGTGC GTGTGTCTCT 1000  
GTCTCTCCTA GCCCCTCTCT CACACATCAC ATTCCCATGG TGGCTCAAG 1050  
AAAGGCCCGG AAGCCCCAGG CTGGAGATAA CAGCCTCTTG CCCGTCGGCC 1100  
CTGCGTCGGC CCTGGGGTAC CATGTGCCAC AACTGCTGTG GCCCCCTGTC 1150  
CCCAAGACAC TTCCCTTGT CTCCCTGGTT GCCTCTCTTG CCCCTTGTCC 1200  
TGAAGCCCAG CGACACAGAA GGGGGTGGGG CGGGTCTATG GGGAGAAAGG 1250  
GAGCGAGGTC AGAGGAGGGC ATGGGTGGGC AGGGTGGGCG TTTGGGGCCC 1300  
TCATGCTGGC TTTTCACCCC AGAGGACACA GGCAGCTTCC AAAATATATT 1350  
TATCTTCTTC ACGGGAAAAA AAAAAAAAAA ACCG 1384

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val  
 1 5 10  
 Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu  
 15 20 25  
 Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser  
 30 35 40  
 Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys  
 45 50 55  
 Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn  
 60 65 70  
 Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys  
 75 80  
 Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala  
 85 90 95  
 Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly  
 100 105 110  
 Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser  
 115 120 125  
 Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn  
 130 135 140  
 Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr  
 145 150  
 Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg  
 155 160 165  
 Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His  
 170 175 180  
 Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg  
 185 190 195  
 Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala  
 200 205 210  
 Leu Arg Leu Glu Leu Leu Gly Cys  
 215

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly  
 1 5 10  
 Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr  
 15 20 25  
 Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys  
 30 35 40  
 His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu  
 45 50 55  
 Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser  
 60 65 70  
 Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr  
 75 80  
 Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg  
 85 90 95  
 Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser

100						105						110		
Tyr	Gly	Asn	Asp	Gln	Trp	Leu	Gln	Val	Asp	Leu	Gly	Ser	Ser	
		115					120					120		
Lys	Glu	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asn	Phe	
			130					135					140	
Gly	Ser	Val	Gln	Phe	Val	Ala	Ser	Tyr	Lys	Val	Ala	Tyr	Ser	
				145					150					
Asn	Asp	Ser	Ala	Asn	Trp	Thr	Glu	Tyr	Gln	Asp	Pro	Arg	Thr	
155					160					165				
Gly	Ser	Ser	Lys	Ile	Phe	Pro	Gly	Asn	Trp	Asp	Asn	His	Ser	
	170					175					180			
His	Lys	Lys	Asn	Leu	Phe	Glu	Thr	Pro	Ile	Leu	Ala	Arg	Tyr	
		185					190					195		
Val	Arg	Ile	Leu	Pro	Val	Ala	Trp	His	Asn	Arg	Ile	Ala	Leu	
			200					205					210	
Arg	Leu	Glu	Leu	Leu	Gly	Cys								
				215		217								

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Phe	Lys	Gly	Asn	Ser	Thr	Arg	Asn	Val	Met	Tyr	Phe	Asn	Gly
1				5					10				
Asn	Ser	Asp	Ala	Ser	Thr	Ile	Lys	Glu	Asn	Gln	Phe	Asp	Pro
15					20					25			
Pro	Ile	Val	Ala	Arg	Tyr	Ile	Arg	Ile	Ser	Pro	Thr	Arg	Ala
	30					35					40		
Tyr	Asn	Arg	Pro	Thr	Leu	Arg	Leu	Glu	Leu	Gln	Gly	Cys	Glu
		45					50					55	
Val	Asn	Gly	Cys	Ser	Thr	Pro	Leu	Gly	Met	Glu	Asn	Gly	Lys
			60					65					70
Ile	Glu	Asn	Lys	Gln	Ile	Thr	Ala	Ser	Phe	Lys	Lys	Ser	
			75					80					
Trp	Trp	Gly	Asp	Tyr	Trp	Glu	Pro	Phe	Arg	Ala	Arg	Leu	Asn
85				90					95				
Ala	Gln	Gly	Arg	Val	Asn	Ala	Trp	Gln	Ala	Lys	Ala	Asn	Asn
100					105				110				
Asn	Lys	Gln	Trp	Leu	Glu	Ile	Asp	Leu	Leu	Lys	Ile	Lys	Lys
	115					120					125		
Ile	Thr	Ala	Ile	Ile	Thr	Gln	Gly	Cys	Lys	Ser	Leu	Ser	Ser
		130					135					140	
Glu	Met	Tyr	Val	Lys	Ser	Tyr	Thr	Ile	His	Tyr	Ser	Glu	Gln
			145					150					
Gly	Val	Glu	Trp	Lys	Pro	Tyr	Arg	Leu	Lys	Ser	Ser	Met	Val
155					160				165				
Asp	Lys	Ile	Phe	Glu	Gly	Asn	Thr	Asn	Thr	Lys	Gly	His	Val
	170					175				180			
Lys	Asn	Phe	Phe	Asn	Pro	Pro	Ile	Ile	Ser	Arg	Phe	Ile	Arg
		185					190				195		
Val	Ile	Pro	Lys	Thr	Trp	Asn	Gln	Ser	Ile	Ala	Leu	Arg	Leu
			200				205						210

Glu Leu Phe Gly Cys Asp Ile Tyr  
                   215                  218

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 218  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS:  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly  
   1                  5                  10  
 Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro  
  15                  20                  25  
 Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr  
  30                  35                  40  
 Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp  
  45                  50                  55  
 Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala  
  60                  65                  70  
 Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn  
  75                  80  
 Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu  
  85                  90                  95  
 Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro  
  100                 105                 110  
 Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val  
  115                 120                 125  
 Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Glu  
  130                 135                 140  
 Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly  
  145                 150  
 His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val  
  155                 160                 165  
 Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser  
  170                 175                 180  
 Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro  
  185                 190                 195  
 Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu  
  200                 205                 210  
 Gly Cys Glu Ala Gln Asp Leu Tyr  
                   215                  218